

Data Management in Biosciences

What are you trying to achieve in your research?

We deploy portable genomic sequencing in the field to:

- Perform rapid real-time genomic surveillance of infectious diseases.
- Understand the spread of pathogens by sequencing and comparing genomes eg. Ebola and Zika epidemics.

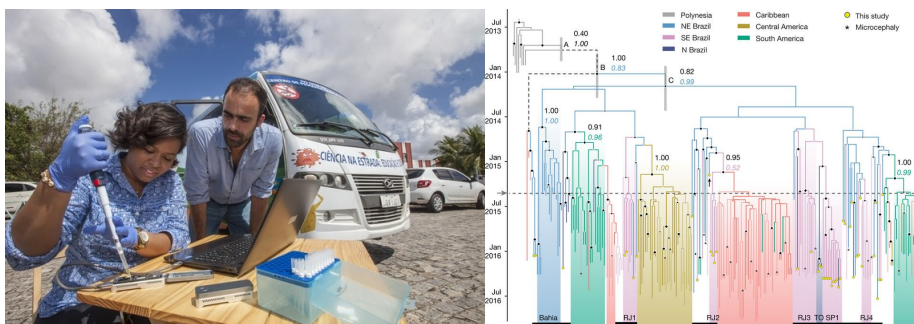
These analyses require:

- Significant CPU power (~240 CPU cores in parallel).
- Vast amounts of storage (~100TB).

Which BEAR Service(s) enable your research?

We use Cloud Infrastructure for Microbial Bioinformatics (CLIMB) [which is a multi-site collaboration between Universities supported through BEAR] to:

- Flexibly increase capacity on demand as we sequence more genomes.
- Reconstruct the pathogen's "family-tree" including accurate dating of introductions into affected region.
- BlueBEAR to process the huge amounts of data.
- BEAR Research Data Store to store the processed data securely, allowing access to all group members.



Left: Using an Oxford Nanopore MinION portable sequencing device in Brazil. **Right:** A family tree of the Zika virus (from Faria et al. 2017, Nature).

Case study



Client Profile

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Funding

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Services Used

CLIMB
BlueBEAR
BEAR Research Data Store

